

PCT09

RAW SEQUENCE LISTING

DATE: 10/23/2001

PATENT APPLICATION: US/09/806,708A

TIME: 10:16:42

Input Set : A:\44137.txt

Output Set: N:\CRF3\10232001\I806708A.raw

3 <110> APPLICANT: The University of British Columbia
 5 <120> TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
 7 <130> FILE REFERENCE: 4810-58741
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/806,708A
 C--> 10 <141> CURRENT FILING DATE: 2001-04-03
 12 <150> PRIOR APPLICATION NUMBER: US 60/147,133
 13 <151> PRIOR FILING DATE: 1999-08-04
 15 <160> NUMBER OF SEQ ID NOS: 23
 17 <170> SOFTWARE: PatentIn version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 12
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Arabidopsis thaliana
 24 <220> FEATURE:
 25 <221> NAME/KEY: misc_signal
 26 <222> LOCATION: (1)..(12)
 27 <223> OTHER INFORMATION: CE3 element at 381-369 bp
 30 <400> SEQUENCE: 1
 31 acacattccc tc
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 12
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial sequence
 39 <220> FEATURE:
 40 <221> NAME/KEY: misc_signal
 41 <222> LOCATION: (1)..(12)
 42 <223> OTHER INFORMATION: consensus sequence
 45 <400> SEQUENCE: 2
 46 acqcggtgtcc tc
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 25
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Artificial sequence
 54 <220> FEATURE:
 W--> 55 <221> NAME/KEY: primer
 56 <222> LOCATION: (1)..(25)
 57 <223> OTHER INFORMATION: AtproFW
 60 <400> SEQUENCE: 3
 61 ctagttagatt ggttggttgg ttcc
 64 <210> SEQ ID NO: 4
 65 <211> LENGTH: 27
 66 <212> TYPE: DNA
 67 <213> ORGANISM: Artificial sequence
 69 <220> FEATURE:
 W--> 70 <221> NAME/KEY: primer
 71 <222> LOCATION: (1)..(27)
 72 <223> OTHER INFORMATION: AtproRV

ENTERED

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12

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75 <400> SEQUENCE: 4
76 tgetctgttt gtgtcggaaa ataattgg 27
79 <210> SEQ ID NO: 5
80 <211> LENGTH: 27
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial sequence
84 <220> FEATURE:
W--> 85 <221> NAME/KEY: primer
86 <222> LOCATION: (1)..(27)
87 <223> OTHER INFORMATION: AP1
90 <400> SEQUENCE: 5
91 ggatcctaatacgaactcact atagggc 27
94 <210> SEQ ID NO: 6
95 <211> LENGTH: 25
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial sequence
99 <220> FEATURE:
W--> 100 <221> NAME/KEY: primer
101 <222> LOCATION: (1)..(25)
102 <223> OTHER INFORMATION: Bnwalk1
105 <400> SEQUENCE: 6
106 aaagagtggagcgatgggta tgagg 25
109 <210> SEQ ID NO: 7
110 <211> LENGTH: 18
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial sequence
114 <220> FEATURE:
W--> 115 <221> NAME/KEY: primer
116 <222> LOCATION: (1)..(18)
117 <223> OTHER INFORMATION: AP2
120 <400> SEQUENCE: 7
121 ctatagggctcgagcggc 18
124 <210> SEQ ID NO: 8
125 <211> LENGTH: 25
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial sequence
129 <220> FEATURE:
W--> 130 <221> NAME/KEY: primer
131 <222> LOCATION: (1)..(25)
132 <223> OTHER INFORMATION: Bnwalk2
135 <400> SEQUENCE: 8
136 cggaaagaagcaaaggttga aaagg 25
139 <210> SEQ ID NO: 9
140 <211> LENGTH: 24
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial sequence
144 <220> FEATURE:
W--> 145 <221> NAME/KEY: primer
146 <222> LOCATION: (1)..(24)

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147 <223> OTHER INFORMATION: Lawalk1
150 <400> SEQUENCE: 9
151 gatacgttttgt ggtaagacga gagc 24
154 <210> SEQ ID NO: 10
155 <211> LENGTH: 24
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial sequence
159 <220> FEATURE:
W--> 160 <221> NAME/KEY: primer
161 <222> LOCATION: (1)..(24)
162 <223> OTHER INFORMATION: Lawalk2
165 <400> SEQUENCE: 10
166 gtcagtggga agaaacagag qttg 24
169 <210> SEQ ID NO: 11
170 <211> LENGTH: 25
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial sequence
174 <220> FEATURE:
W--> 175 <221> NAME/KEY: primer
176 <222> LOCATION: (1)..(25)
177 <223> OTHER INFORMATION: BnproFW
180 <400> SEQUENCE: 11
181 ctgacttcac caaagaaaca actcg 25
184 <210> SEQ ID NO: 12
185 <211> LENGTH: 26
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial sequence
189 <220> FEATURE:
W--> 190 <221> NAME/KEY: primer
191 <222> LOCATION: (1)..(26)
192 <223> OTHER INFORMATION: BnproRV
195 <400> SEQUENCE: 12
196 cgggaattccg tttttttttt taggcg 26
199 <210> SEQ ID NO: 13
200 <211> LENGTH: 23
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial sequence
204 <220> FEATURE:
W--> 205 <221> NAME/KEY: primer
206 <222> LOCATION: (1)..(23)
207 <223> OTHER INFORMATION: LaproFW
210 <400> SEQUENCE: 13
211 cagcttaacc ggtaaaattg gcc 23
214 <210> SEQ ID NO: 14
215 <211> LENGTH: 23
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial sequence
219 <220> FEATURE:
W--> 220 <221> NAME/KEY: primer

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221 <222> LOCATION: (1)..(23)
222 <223> OTHER INFORMATION: LaproRV
225 <400> SEQUENCE: 14
226 ttttcagttt tgtgtcggag agg                23
229 <210> SEQ ID NO: 15
230 <211> LENGTH: 393
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial sequence
234 <220> FEATURE:
235 <221> NAME/KEY: promoter
236 <222> LOCATION: (1)..(393)
237 <223> OTHER INFORMATION: transcriptional regulatory region
240 <400> SEQUENCE: 15
241 agatctaaga acacacattc cctcaaattt taatgcacat gtaatcatag tttagcaciaa        60
243 ttcaaaaaata atgtagtatt aaagacagaa atttgtagac ttttttttgg cgtaaaggga        120
245 aqactaagtt tatacgtaca ttttatttta agtggaaaac cgaaattttc catcgaaaata        180
247 tatqaattta gtatatatat ttctgcaatg tactattttg ctattttggc aactttcagt        240
249 ggaactactac tttattacaa tgtgtatgga tgcattgatt tgagtataca catgtctaaa        300
251 tgcattgcttt gcaaaacgta acggaccaca aaagaggatc catgcaaata catctcatag        360
253 ctctctccat tattttccga cacaacacaga gca                393
256 <210> SEQ ID NO: 16
257 <211> LENGTH: 900
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial sequence
261 <220> FEATURE:
262 <221> NAME/KEY: promoter
263 <222> LOCATION: (1)..(900)
264 <223> OTHER INFORMATION: transcriptional regulatory region
267 <400> SEQUENCE: 16
268 aaggcttacc ctattagttg aaagttgaaa ctttgttccc tactcaattc ctagttgtgt        60
270 aaatgtatgt atatgtaatg cgtataaaac gtagtactta aatgactagg agtggttcctt        120
272 gagaccgatg agagatggga gcagaactaa agatgatgac ataattaaga acgaatttga        180
274 aaggctotta ggtttgaatc ctattcgaga atgtttttgt caaagatagt ggcgattttg        240
276 aaccaaagaa aacatttaaa aaatcagtat ccggttacgt tcatgcaaat agaaaagtgg        300
278 ctaggatctg attgtaattt tagacttaaa gagtctctta agattcaatc ctggctgtgt        360
280 acaaaaactac aaataatata ttttagacta tttggcctta actaaacttc cactcattat        420
282 ttactgaggt tagagaatag acttgcgaaat aaacacattc ccgagaaaata ctcatgatcc        480
284 tataattagt cagagggtat gccaatcaga tctaagaaca cacattccct caaattttaa        540
286 tgcacatgta atcatagttt agcacaattc aaaaataatg tagtattaaa gacagaaatt        600
288 tqttagacttt tttttggcgt taaaggaaga ctaagtttat acgtacattt tattttaagt        660
290 qgaaaaccga aattttccat cgaaatatat gaatttagta tatatatttc tgcaatgtac        720
292 tattttgcta ttttggaac tttcagtggg ctactacttt attacaatgt gtatggatgc        780
294 atgagtttga gtataacat gtctaaatgc atgctttgca aaacgtaacg gaccacaaaa        840
296 gagqatccat gcaaatacat ctcatagctt cctccattat tttccgacac aaacagagca        900
299 <210> SEQ ID NO: 17
300 <211> LENGTH: 1588
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial sequence
304 <220> FEATURE:

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395 <221> NAME/KEY: promoter
396 <222> LOCATION: (1)..(1588)
397 <223> OTHER INFORMATION: transcriptional regulatory region
398 <400> SEQUENCE: 17
399 ctgacttcac caaagaaaca actcgagtcg ttatccatct cctcataacc atcgctccac      60
400 tctttgcctt caccgttttc ggttcgggtt ttacatcgcc aaccgcggcc aaaccgggtt      120
401 acctcggttg gtactcatgc taccttcac caacgcattg tagatcaagt atctccaagg      180
402 tcatggatat cttttatcaa gtaagaaaag ctgactcttc tcggaacggc acgtgcgatg      240
403 actcgctgtg gcttgacttc ttgaggaaga ttcaagaacg ttcaggtcta ggcatgaaa      300
404 ctcaacggcc cgaggggctg cttcagggtc ctcacgggaa gacttttgcg gcggcgcggtg      360
405 aaagacggga gcaagttatc attggtgcgc tagaaaatct attcaagaac accaacgtta      420
406 acctaaaga tataggtata cttgtggtga actcaagcat gtttaatcca actccatcgc      480
407 tctcgcgat ggtcgtaaac actttcaagc tccgaagcaa cgtaagaagc tttaaccttg      540
408 gtggcatggg ttgtagtgcg ggcgttatag ccattgatct agcaaaggac ttgttgcgat      600
409 tccataaaaa tacgtatgct cttgtggtga gcacagagaa catcacttat aacatttacg      660
410 ctggtgataa taggtccatg atggtttcaa attgcttggt cegtgttgtt ggggccgcta      720
411 ttttgccttc caacaagcct ggagatcgta gacgggtccaa gtacgagcta gttcacacgg      780
412 ttgaacgca taccggagct gacgacaagt cttttcggtt cgtgcaacaa ggagacgatg      840
413 agaacggcaa aatcgaggtg agtttgtcca aggacataac cgatgttget ggtcgaacgg      900
414 ttaagaaaaa catagcaacg ttgggtccgt tgattcttcc gtttaagcag aaacttcttt      960
415 ttttcgttac cttcatgggc aagaaacttt tcaagataa aatcaaacat tactacgtcc      1020
416 cggatttcaa acttgcattt gaccattttt gtatacatgc cggaggcaga gccgtgattg      1080
417 atgtgctaga gaagaacctt gccctagcac cgatcgatgt agaggcatca agatcaacgt      1140
418 tacaatagatt tggaaacctt tcatctagct caatatggta tgagttggca tacatagaag      1200
419 caaaagggaag gatgaagaaa ggtaataaag tttggcagat tgctttaggg tcagggttta      1260
420 agtgtaacag tgcagtttgg gtggtctctaa acaatgtcaa agcttcgaca aatagtcctt      1320
421 ggaacactg catcgacaga taccgggtca aaattgattc tgattcaggt aagtcagaga      1380
422 ctggtgtcca aaacggtcgg tcttaataaa cgatgtttgc tctctttcgt ttctttttat      1440
423 ttgttataat aatttgatgg ctacgatgtt tctcttggtt gttatgaata aagaatgcaa      1500
424 tgggtttcta gtatttgatt gttttacatg tatgtatctc ttattttacat gaaattttta      1560
425 aacgcctaaa aaaaaaacg gaattccg                                1588
396 <210> SEQ ID NO: 18
397 <211> LENGTH: 1069
398 <212> TYPE: DNA
399 <213> ORGANISM: Artificial sequence
399 <220> FEATURE:
399 <221> NAME/KEY: promoter
399 <222> LOCATION: (1)..(1069)
399 <223> OTHER INFORMATION: transcriptional regulatory region
399 <400> SEQUENCE: 18
399 cagcttaacc ggtaaaattg gcctgtacat atatttacca ctgagtaaag acatcagtta      60
399 atgatttgtt gttactcaat tgggctaagt gtattattat atgtgttgta tataataaag      120
399 gtgaacgcta aatttactaa gaatgtgttt ttccaatgtg attgctcttt ggctcttag      180
399 gtttgaatcc tactcgagaa gactaatttt aatttactgg caaaaataga aatcaattta      240
399 taagtgttta aacaaatcga tgggtataact gattagtgat cactcttagg ttttgatcca      300
399 actcgagtat tgagtattga acgctttttt taaataaaat cttgattttt aaattgggtt      360
399 tttagtataa aaagttctta atattttctc tttgttttaa tgggtttgtt ttgcatttta      420
399 taagcttaat ttttctaatt taatatttta tctatcatcg tccgtaaagt tttatttggc      480
399 acaaacttgt tttacttttc taccttataa tttgggaact ggttgagtca aagcgtaccg      540

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\44137.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:55 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:70 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:85 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:130 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:145 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:160 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:175 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:190 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:205 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:220 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

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L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23